



axmi006	-----MNQNNNDNNEYEIIDSHSTSPYFPNRRNSNDSRYPYTNNPNQPLQNTNYKEWLNMCQGN	56
cry1Aa	-----MDNNPNINECIPYN---CLSNPE-----VEVL	24
cry1Ac	-----MDNNPNINECIPYN---CLSNPE-----VEVL	24
cry1Ia	-----MKLKNQDKHQSFSSNAKVDKISTDS---LKNETDIELQININHEDCLKMSEYE	49
cry3Aa1	MIRKGGGRKMNNRSEHDTIKTTENNEVPTNHVQYPLAETPNPTLEDLNYKEFLRMTADN	60
cry3Ba	MIRMGGGRKMNNRSEYDTIKVTPNSELPTNHNQYPLADNPNSTLEELNYKEFLRMTADN	60
cry4Aa	----MNPYQNKNEYETLN--ASQKKLNISNNYTRYPIENSPKQLLOSTNYKDWLNMCQGN	54
cry6Aa	-----MNLNNLD--GYEDSNRTLNNLSLNY--TQKALSPSLKNNYQDFLSITERE	47
cry7Aa	-----MSPNNQNEYEIIDATPSTSVSSDSNRYPFANEPTDALQNNMYKDYLMKSGGE	52
cry8Aa	----MNPYQNKNEYEIFN--APSNFSGSKNNYSRYPLANKPNQPLKNTNYKDWLNVCQDN	54
cry10Aa	----MHYYGNRNEYDILN--ASSNDSNMSNTYPRYPLANPQODLMQNTNYKDWLNVCQDN	54
cry16Aa	----MNSYQNKNEYEILD--AKRNTCHMSNCPKYPLANDPQMYLRNTHYKDWLNVCQDN	54
cry19Ba	----MNSYQNKNEYEILD--AKRNTCHMSNCPKYPLANDPQMYLRNTHYKDWLNVCQDN	54
cry24Aa	----MNQYQNKNEYEILE-----SSQNNMMPNRYPFADDPNAVMMKNGNYKDWVNECEGS	51

axmi006	TQYGDNFETFASADTIAAVSAGTIVSGTLLAGIGGLTSISGPIGIIIGAIISFGTLIT--	114
cry1Aa	G-----GERIETGYTPIDISLSLTQFLLSEF-VPGAGFVLG-----LVDIIWG--	66
cry1Ac	G-----GERIETGYTPIDISLSLTQFLLSEF-VPGAGFVLG-----LVDIIWG--	66
cry1Ia	N-----VEPFVS-ASTIQTGIGIAGKILGTLGVFPFAGQVAS-----LYSFILG--	91
cry3Aa1	N-----TEALDSSTTKDVIQKGISVVGDLGVLGVFPFAGALVS-----FYTNFLN--	105
cry3Ba	S-----TEVLDSSTVKDAVGTGISVVGQILGVGVFPFAGALTS-----FYQSFLN--	105
cry4Aa	QQYGGDFETFIDSG---ELSAITIVVGTVLTGFGFTTPLG-----LALIGFGTLIP--	102
cry6Aa	-----MIIDSKTTLPRHSLIHTIKLNSNKKYGPDMTN-----GNQFIISKQ	42
cry7Aa	Q-----PEALASGNTAINTVSVVTGATLSALGVPGASFITN-----FYLKIAG--	90
cry8Aa	NP-ELFGNPETFIS-SSTIQTGIGIVGRILGALGVFPFASQIAS-----FYSFIVG--	100
cry10Aa	QQYGNAGNFASSETIVGVSAIIIVGTMLGAFAAPVLAAG-----IISFGTLLP--	104
cry16Aa	H-----IENPREASVRAGLGKGLGIVSTIVGFFGGSIIILDTIG-----LFYQISE--	99
cry19Ba	S-----YASSGPSQL---FKVGGSIIVAKILG-----MIPEVGP-----LLSWMVS--	91
cry24Aa	N-----ISPSPAAAITSKIVSIVLKTAKAVASSLAD-----SIKSS--	88

axmi006	VFWPAGEQDKTVWTQFIKMGEIFVDTPLTESIKQLKLQTLLEGFRQILQ-SYNTALDDWRK	173
cry1Aa	IFGPS--Q---WDAFPVQIEQLINQRIEEFARNQAISRLEGLSNLYQ-IYAESFREWEA	119
cry1Ac	IFGPS--Q---WDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQ-IYAESFREWEA	119
cry1Ia	ELWP---KGKNQWEIFMEHVEEIIINQKISTYARNKALTDLKGLGDALA-VYHDSLESWVG	147
cry3Aa1	TIWPS--E--DPWKAFMEQVEALMDQKIADYAKNKALAEQGLQNNVE-DYVSALSSWQK	160
cry3Ba	AIWPS--DA-DPWKAFMAQVEVLIDKKIEEYAKSKALAEQGLQNNFE-DYVNALDSWKK	161
cry4Aa	VLFPAQDQS-NTWSDFITQTKNIIKKEIASTYISNANKILNRSFNVIS-TYHNHLKTWE-	159
cry6Aa	E-----WATIGAYIQTGLGLPVNEQQRLRTHVNLSQDISIPSD--FSQLYDVYCS	89
cry7Aa	LLWPE--NGKI-WDEFMTEVEALIDQKIEEYVRNKAIAELDGLGSALD-KYQKALADWLG	146
cry8Aa	QLWPS--KSVDIWGEIMERVEELVDQKIEKYVKDKALAEKGLGNALD-VYQOSLEDWLE	157
cry10Aa	IFWQGS DPA-NVWQDLLNIGGRPIQ-EIDKNIINVLTISIVTPIKNQLD-KYQEFFDKWEP	161
cry16Aa	LLWPEDDTQQYTWQDIMNHVEDLIDKRITVIRGNARTLADLQKVD-DYNNWLKKWKD	158
cry19Ba	LFWPTIEEKNVWEDMIKYVANLLKQELTNDTLNRATSNLSGLNESLN-IYNRALAAWKQ	150
cry24Aa	LGISKTITENNVSQVSMVQVHQIINRRIQETILDLGESSLNLGLVAIYNRDYLGALAEAWN	148

Fig. 1A

Application No: 10/783,417
Amendment Dated: May 12, 2006
Reply to Office Action of February 16, 2006
REPLACEMENT SHEET

axmi006 LKRLQAPGLPPSSALQQAALTLKIRFENVHNDFFIREIPG--FQLETYKTL LLPIYAQAAN 231
cry1Aa -----DPT---NPALREEMRIQFNDMNSALTTAIPLLAVQ-----NYQVPLLSVYVQAAN 166
cry1Ac -----DPT---NPALREEMRIQFNDMNSALTTAIPLFAVQ-----NYQVPLLSVYVQAAN 166
cry1Ia -----NRN---NTRARSVVKSQYIALELMFVQKLP SFAVS-----GEEVPLLP IYAQAAN 194
cry3Aa1 -----NPVSSRNPHSQGRIRELFSQAESHFRNSMPSFAIS-----GYEVLFLLT TYAQAAN 210
cry3Ba -----APVNLRSRRSQDRIRELFSQAESHFRNSMPSFAVS-----KFEVLFLLPT YAQAAN 211
cry4Aa ----NNPNPQNTQDVRTQIQLVHYHFQNVIPELVNSCPPNPSCDYNNILVLSSYAQAAN 215
cry6Aa -----DKTSAEWWNK NLYPLIIKSANDIASY-----GFKVAGDPSIKKDG- 129
cry7Aa -----KQD---DPEAILS VATEFRIIDSLFEFSMPSFKVT-----GYEIPLLTVYAQAAN 193
cry8Aa -----NRN---DARTRSVVSNQFIALDLNFVSSIPSFAVS-----GHEVLLLAVYAQAAN 204
cry10Aa -----ARTHANAKAVHDLFTTLEPIIDKDLMLKN---NASYRIPTLPAYA QIAT 208
cry16Aa ----DPKSTGNLSTLVTKFTALDSDFNGAIRTVNNQGSF-----GYELLLL PVYAQIAN 208
cry19Ba ----NKNNFASGELIRSYINDLHILFTRDIQSDFSLG-----GYETVLLPSYASAAN 198
cry24Aa -----NKSININYQTNVAEAFKTVEREFFTKLKG IYRTS----SSQITLLPTFTQAAN 196

axmi006 FHLNLLQQAELADEWNADIIHPSQIEPNAGTSDDYYK-LLKENIPKYSNYCANTYRTGLK 290
cry1Aa LHLSVLRDVSFVGQRWGFDA-----ATINSRYNDLTRLIGNYTDYAVRWYNTGLE 216
cry1Ac LHLSVLRDVSFVGQRWGFDA-----ATINSRYNDLTRLIGNYTDYAVRWYNTGLE 216
cry1Ia LHLLLLRDASIFGKEWGLSS-----SEISTFYNRQVERAGDYS DHCVKWYSTGLN 244
cry3Aa1 THLFLLKDAQIYGEEWGYEK-----EDIAEFYKRQLKLTQ EYTDHCVKWYNVGLD 260
cry3Ba THLLLLLKDAQVFGEWGYSS-----EDIAEFYQRQLKLTQ QYTDHCVNWYNVGLN 261
cry4Aa LHLTVLNQAVKFEAYLKNNRQFDYLEPLP-TAIDYYP-VLT KAIEDYTNVCVTTYKKGLN 273
cry6Aa -YFKKLQDELDNIVDNNSSD-----DAIAKAIKDFKARC GILIKEAKQ 171
cry7Aa LHLALLRDSTLYGDKWGFTQ-----NNIEENYNRQKKRI SEYSDHCTKWYNSGLS 243
cry8Aa LHLLLLRDASIFGEEWGFTP-----GEISR FYNRQVQLTAEYSDYCVKWYKIGLD 254
cry10Aa WHLNLLKHAATYYNIWLQN---QGINPSTFNSSNYYQGYLKR KIQEYTDYCIQTYNAGLT 265
cry16Aa LHLLLLRD AQIYGDKWWSAR-----ANARDNYYQIQLEK TKEYTEYCINWYNKGLN 259
cry19Ba LHLLLLRDVAIYG-KELGYP-----STDVEFYNEQKY YTEKYSNYCVNTYKSGLE 248
cry24Aa LHL SMLRDAVMYQEGWNLQS-----HINYSKELDDALED YTNVCVEVYTKGLN 244
:: *..

axmi006 NLRDEP-----NMKWSIFNDYRRYMTITVLDTISQFSLYDIKRYRDSIGGIEVKGIKNE 344
cry1Aa RVWGPDS-----RDWVRYNQFRRELTLTVLDIVALFSNYDSRRYP-----IRTVSQ 262
cry1Ac RVWGPDS-----RDWVRYNQFRRELTLTVLDIVALFPNYDSRRYP-----IRTVSQ 262
cry1Ia NLRGTNA-----ESWVRYNQFRDMTLMVLDLVALFPSYDTQ MYP-----IKTTAQ 290
cry3Aa1 KLRGSSY-----ESWVNFNRYRREMTLTVLDLIALFPLYD VRLYP-----KEVKTE 306
cry3Ba SLRGSTY-----DAWVKFNRFRRMTLTVLDLIVLF PFYDVRLYS-----KGVKTE 307
cry4Aa LIKTT PDSNLDGNINWNTYNTYRTKMTTAVLDLVALFPNYDVGKYP-----IGVQSE 325
cry6Aa YEEAAKN-----IVTSLDQFLHGDQKKLEG----- 196
cry7Aa RLNGSTY-----EQWINYNRFRREMILMALDLVAVFPFHD PRRYS-----METSTQ 289
cry8Aa KLKGTT S-----KSWLNHYHQFRREMTLLVLDLVALFPNYDTHMYP-----IETTAQ 300
cry10Aa MIRTNT-----NATWNMYNTYRLEMTLTVLDLIAIFPNYD PEKYP-----IGVKSE 311
cry16Aa DFRTAGQ-----WVNFNRYRREMTLTVLDIISMFP IYDARLYPT-----EVKTE 303
cry19Ba SKKQIG-----WSDFNRYRREMTLSVLDIVALFPLYDTGLYPSKDGK---IHVKAE 296
cry24Aa ALRGSTA-----IDWLEFNSFRDMTLMVLDLVAIFPNYNPV RYP-----LSTKIS 290
: : * :

Fig. 1B

axmi006	LTREIYTTTEINFDRLPQLR-----VQPNLATMEYNLTRASFKLFSFLEQFIFYTENTN	397
cry1Aa	LTREIYTNPVLENFDGS-----FRG--MAQRIEQNIRQPHLMDILNSITIYTDVHR	311
cry1Ac	LTREIYTNPVLENFDGS-----FRG--SAQGIERSIRSPHLMDILNSITIYTDHR	311
cry1Ia	LTREVYTDAIGTVHPPHSFTSTTWYNNNAPSFSFAIEAAVVRNPHLLDFLEQVTIYSLLS-	349
cry3Aa1	LTRDVLTDPIVGVNNLR-----GYGTTFSNIEN-YIRKPHLFDYLHRIQFHTRFQP	356
cry3Ba	LTRDIFTDPIFTLNLQ-----EYGPFTSSNIEN-SIRKPHLFDYLRGIEFHTRLRP	357
cry4Aa	LTREIY-QVLNFEESEPYK-----YYDFQYQEDSLTRR-PHLFTWLDSLNFYEKAQT	374
cry6Aa	-----VINIQKRLKEVQTALN-----	212
cry7Aa	LTREVYTDPVLSISNP-----DIGPSFSQMENTAIRTPLVDYLDLYIYTSKYK	340
cry8Aa	LTRDVYTDPIAFNIVTSTGFCNPWSTHSGILFYEVENNVRPPHLFDILSSVEINTSRGG	360
cry10Aa	LIREVYTNVNSDT-----FRITELENGLTRN-PTLFTWINQGRFYTRNSR	356
cry16Aa	LTREIYSDVINGEIYGLMT-----PYFSFEKAESLYTRA-PHLFTWLKGFRTVNSIS	355
cry19Ba	LTREIYSDVINDHVYGLMV-----PYISFEHAESLYTRR-PHAFTWLKGFRTVNSIN	348
cry24Aa	LSRKIYTDVPVGRDTPSPFG-DWTNTGRTLAFNDLREVTDSPLVKWLGDMTIYTGAI	349
:		
axmi006	FGN-----RLVGISNRDAPTYSNTITET--LYGERTGSPTTKTIRPFESYKVSIVTD	447
cry1Aa	GFN-----YWSGHQITASPVGFGSGPEFAFPLFGNAGNAAPP-VLVS LTGLGIFRTLS	362
cry1Ac	GYG-----YWSGHQIMASPVGFGSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLS	363
cry1Ia	-RWSNTQYMN-MWGGHKLEFRTIGGTNLISTQ---GSTNTSINPVTLPTSRDVRTE	403
cry3Aa1	GYGNDTSFN--YWSGNYVSTRPSIGSNDIITSPFYGNKSSEPVQ--NLEFNGEKVYRAVA	412
cry3Ba	GYSGKDSFN--YWSGNYVETRPSIGSNDITSPFYGDKSIEPIQ--KLSFDGQKVYRTIA	413
cry4Aa	TPN-----NFFTSHYNMFYHTLDNISQKSSVFGNHNVTDKLKS LG-LATNIYIFLLN	425
cry6Aa	-----QAHGESSPAHKELLEKVKNLKTTLERTIKAEQDLEKKVEY	252
cry7Aa	AFSHEIQPDLFYWSAHKVSFKKSEQSN-LYTTGIYKGTSGYISS-GAYSFHGNDIYRTLA	398
cry8Aa	ITLNDNDAYIN-YWSGHTLKYRRRTADSTVYTA---NYGRITSEKNSFALEDRIFEINS	415
cry10Aa	DIL-----DPYDIFSFTGNQMAFTHTNDNRNIWGAHVGNIIISQDTSKVPFYRNKP	408
cry16Aa	YWT-----FLSGGQNKYSYTN-NSSINEGSFRGQD TDYGGTSS TINIPSN SYVYNLW	406
cry19Ba	SWT-----FLSGGENRYFLTHGEGTIYNGPFLGQDTEYGGTSSYIDISNNSSIYNLW	400
cry24Aa	SYRP-----TSPGDRIGVWYGNINAFYHTGRTDVVMFRQTGDTAYEDPSTFISNILYD	402
:		
axmi006	RQSPVPVSP-IQPHFIINQIELYLN GSSNNTLKYSAGGS--LSNYQNTTFFQFPRKKDCNL	504
cry1Aa	SP---LYRRIILGSGPNNQELFVL DGT EFSFASLT TNLPSTIYRQRTVDSL DVI PPQDN	419
cry1Ac	ST---LYRRPFN-IGINNQQLSVLDGT EFA YG-TSSNLPSAVYRKSGTVDSL DEI PPQNN	418
cry1Ia	LAGLNLFLTQPVNGVPRVDFHWKFVTHPIASDNFYYPGYAGIG--TQLQDSENELPPEAT	461
cry3Aa1	NTNLAVWP-SAVYSGVTKEVFSQYNDQTD EAS TQTYDSKR N-VGAV-SWDSIDQLPPETT	469
cry3Ba	NTDIAAFPDGKIYFGVTKVDFSQYDDQKNETSTQTYDSKRY-NGYLGAQDSIDQLPPETT	472
cry4Aa	VISLDNKY-LNDYNNISKMDFFITNGTRLLEKELTAGSGQITYDVNKNIFGLPILKRREN	484
cry6Aa	SFLLGPLLGFVVYEILENTAVQHIKNQIDEIKKQLDSAQHDLDRDVKIIGMLNSINTDID	312
cry7Aa	APSVVVYPYTQN-YGVEQVEFYGVKGHVHYRGDNKYDL-----TYDSIDQLPPDGE	448
cry8Aa	TVANLANYYYQKAYGVPGSWFHMKRGTSSTTAYLYSKTHTALQCTQVYESSDEIPLDRT	475
cry10Aa	IDKVEIVR-HREYSDIIEYEMIFFSNSSE--VFRYSSNSTIENNYKRTDSYMPKQTWKN-	464
cry16Aa	TENYEIYPWGDVPNITKMNFSVTDNNSKELIYGAHRTNKPVVRTDFDFTLNKEGTEL-	465
cry19Ba	TKNYEWIYPWTDVPNITKINFSITDNSNSSES IYGAERMNKPTVRTDFNLLNRAGNGP-	459
cry24Aa	DIYKLDLRAAAVSTIQGAMDTTFGVSSSRFFDIRGNQLYQSNKPYPSPLPITITFPGEES	462

Fig. 1C

axmi006	VIDPGCSPNFNNYSHILSHFSLFTYSYVIGLQLQILDGTGVLGWTSSVDRYNAISDKIIT	564
cry1Aa	S-----VPPRAGFSHRLSHVTMLSQAAG---AVYTLRAPTFWSQHRSAEFNIIIPSSQIT	471
cry1Ac	N-----VPPRQGFSHRLSHVSMFRSGFSNS-SVSIIRAPMFWSIHRSAEFNNIIASDSIT	472
cry1Ia	G-----QPNYESYSHRLSHIGLISASHVK--ALVYS-----WTHRSADRTNTIEPNSIT	508
cry3Aa1	D-----EPLEKGYSHQLNRYVMCFMQGSR-----GTIPVLTWTHKSVDFNMDSSKKIT	518
cry3Ba	D-----EPLEKAYSHQLNYAECFLMQDRR-----GTIPFFTWTTHRSVDFNTIDAEEKIT	521
cry4Aa	QGNPTLFPTYDNYSHILSFIKSLIPATY-----KTQVYTFAWTHSSVDPKNTIYTHLTT	539
cry6Aa	N-----LYSQGQEAIKVFQKLQG-----IWATIGAQIENLRRTTSLQE	349
cry7Aa	-----PIHEKYTHRLCHATAIFKSTP---DYDNATIPIFSWTHRSAEYNNRIYPNKIT	498
cry8Aa	-----VPVAESYSHRLSHITSHSFSKNG--SAYYGSFPVFWTHTSADLNNTIYSDKIT	527
cry10Aa	-----EEYGHTLSYIKTDNYIFSVVR---ERRRVAFSWTHTSVDFQNTIDLDNIT	511
cry16Aa	-----AKYNDYNHILSYMLINGETFGQ----KRHGYSFAFTHSSVDPNNTIAANKIT	513
cry19Ba	-----TTYNDYNHILSYMLINGETFGQ----KRHGYSFAFTHSSVDRYNTIVDPKIV	507
cry24Aa	S-----EGNANDYSHLLCDVKILQEDSSN-ICEGRSSLLSHAWTHASLDRNNTILPDEIT	516
	: : : : *	
axmi006	MIPAIKGNLDTNSKVIIEGPGHTGGNLVYLSQGR-----LEITCETPNSTQSYFIRL	617
cry1Aa	QIPLTKSTNLGSGTSVVKPGPGFTGGDILRRTSPGQISTLRVNITAPL-----SQRYRVRI	526
cry1Ac	QIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRI	531
cry1Ia	QIPLVKAFNLSSGAADVVRGPGFTGGDILRRTNTGTFGDIRVNINPPF-----AQRYRVRI	563
cry3Aa1	QLPLVKAYKLQSGASVVAGPRFTGGDIIQCTENG----SAATYVTP-DVSYSQYRARI	573
cry3Ba	QLPVVKAYALSSGASIIIEGPGFTGGNLLFLKSSN---SIAKFKVTLNSAALLQRYRVRI	578
cry4Aa	QIPAVKANSLGTASKVVQPGPGHTGGDLIDFKDH-----FKITCQHSNFQQSYFIRI	590
cry6Aa	VQSDDDADEIQIELEDASDAWLVAQEAR-----DFTLNAYSTNSRQNLPI	395
cry7Aa	KIPAVKMYKLDDPSTVVKPGPGFTGGDLVKGSTGYIGDIKATVNSPL-----SQRYRVRI	553
cry8Aa	QIPAVKGDMLYLGGSVVQPGPGFTGGDILKRTNPSILGTFAVTVNGSL-----SQRYRVRI	582
cry10Aa	QIHALKALKVSSDSKIVKPGPGHTGGDLVILKDSMD-----FRVRFLKN-VSRQYQVRI	563
cry16Aa	QIPVVKASSINGSISIEKPGPGFTGGDLVKMRADSG-----LTMRFKAELLDDKKYRVRI	566
cry19Ba	QIPAVKTNLVG--ANIIEKPGHTGGDILLKLEYERF-----LSLRIK-LIASMTFRIRI	557
cry24Aa	QIPAVTAYELRGNSSVVGPGSTGGDLVKMSYHS-----VWSFKVYCSSELKNYRVRI	568
	: . . . :	:
axmi006	RYATNGAGNTLPNISLTIPGVIGIPPQRLNNTFSGTNYNNLQYGDGFGYFQFPSTVTPLPLN	677
cry1Aa	RYASTTNLQFHTSIDGRPINQGNFS-----ATMSSGSNLQSGSFRTVGFTTTFNFSNG	579
cry1Ac	RYASVTPIHLNVNWGNSSIFSNTVP-----ATATSLDNLQSSDFGYFESANAFTSSLG	584
cry1Ia	RYASTTDLQFHTSINGKAINQGNFS-----ATMNRGEDLDYKTFRTVGFTTTFPSFLDV	616
cry3Aa1	HYASTSQITFTLSLDGAPFNQYYFD-----KTINKGDTLTYNSENLASFSTPFELSG-	625
cry3Ba	RYASTTNLRLFVQNSNNDFLVIYIN-----KTMNIDGDLTYQTFDFATSNNSMGFSGD	631
cry4Aa	RYASNGSANTRAVINLSIPGVAELG-MALNPTFSGTDYTNLKYKDFQYLEFSNEVKFAPN	649
cry6Aa	NVISDSCNCSTTNMTSNQYSN-----PTTNMTSNQYMISHEYTSLPNFMLSRN	444
cry7Aa	RYATNVSGQFNVYINDKITLQTKFQN---TVETIGEGKDLTYGSFGYIEYSTTIQFPDE	609
cry8Aa	RYASTTDFEFTLYLG-DTIEKNRFN-----KTMNNGASLTETFKFASFITDFQFRET	634
cry10Aa	RYATNAPKTTVFLTGIDTISVELPS---TTSRQNPATDLTYADFGYVTFPRTVPNKTF	619
cry16Aa	RYKCNYSKILRLKWKGEYIQQOI-----HNISPTYGAFSYLESFTITTTENIFDLTM	620
cry19Ba	RYASNISGQMMINIGYQNPTYFNII-----PTTSRDYTELK-FEDFQLVDTSYIYSGGP	610
cry24Aa	RYASHGNCQFLMKRWPSTGVAPRQWAR---HNVQGTFSNSMRYEAFKYLDIFTITPEENN	625

Fig. 1D

axmi006	R--NIPFIFNRADVSN-SILIIDKIEFIPITSSMHQNRKQKLETIQTKINTFFTNHTKT	734
cry1Aa	S---SVFTLSAHVFNSGNEVYIDRIEFVPAEVTFEA---EYDLERAQKAVNELFTSSNQI	633
cry1Ac	N-----IVGVRNFSGTAGVIIDRFEFIPVTATLEA---EYNLERAQKAVNALFTSTNQL	635
cry1Ia	Q---STFTIGAWNFSGNEVYIDRIEFVPVEVTYEA---EYDFEKAQEKVTALFTSTNPR	670
cry3Aa1	----NNLQIGVTGLSAGDKVYIDKIEFIPVN-----	652
cry3Ba	T---NDFIIGAESFVSNEKIYIDKIEFIPVQ-----	659
cry4Aa	Q--NISLVFNRSVDVYTNNTVLIDKIEFLPITRSIREDREKQKLETVQQIINTFYANPIKN	707
cry6Aa	S-----NLEYKCPENNFMIIYWYNNNSDWYNNNSDWYNN-----	475
cry7Aa	H---PKITLHLSDLSSNNSSFYVDSIEFIPVDVNYAE---KEKLEKAQKAVNTLFTE-GRN	662
cry8Aa	Q---DKILLSMGDFSSGQEVYIDRIEFIPVDETYEA---EQDLEAAKKAVNALFTNTKD-	687
cry10Aa	EGEDTLLMTLYGTPNHSYNIYIDKIEFIPITQSVLDYTEKQNIKTQKIVNDLFDVN----	675
cry16Aa	E-VTYPYGRQFVEDIPS--LILDKIEFLPTN-----	648
cry19Ba	S-ISS--NTLWLDNFSNGPVIIDKIEFIPLGITLNAQAGYDITYDQANANGMYHQNYNSNGY	667
cry24Aa	F-----AFTIDLES GGDLFIDKIEFIPVSGSAFEYEGKQNIKTQKAVNDLFIN----	674
	: ::	
axmi006	L-----	735
cry1Aa	GLKTDVTDYHIDQVSNLVECLSDEFCLDEKQELSEKVKHAKRLSDERNLLQDPNFRGINR	693
cry1Ac	GLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINR	695
cry1Ia	GLKTDVKDYHIDQVSNLVESLSDEFYLDEKRELFEIVKYAKQLHIERNM-----	719
cry3Aa1	-----	
cry3Ba	-----	
cry4Aa	TLQSELTDYDIDQAANLVECISEELYPKEKMLLLDEVKNAKQLSQSRNVLQNGDFE----	763
cry6Aa	-----	
cry7Aa	ALQKDVTDYKVDQVSILVDCISGDLYPNEKRELQNLVKYAKRLSYSRNLLLDPTFDSINS	722
cry8Aa	GLRPGVTDYEVNQAANLVECLSDDLYPNEKRLLFDVREAKRLSGARNLLQDPDFQEING	747
cry10Aa	-----	
cry16Aa	-----	
cry19Ba	NYNQEYNTYYQSYNN-----	682
cry24Aa	-----	

Fig. 1E